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processes in a species-specific manner.

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Toward a characterization of the pepper host resistance effect on the gene expression of the pathogenic *Phytophthora capsici*

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The Oomycete *Phytophthora capsici* is a polyphagic pathogen which attacks various plant species of agronomic interest. It is notably known to cause important damages on pepper. A few partially resistant pepper genitors have been described and to identify the effect of the pepper resistance on the gene expression of *P. capsici*, a RNA-Seq analysis was used. Two pepper accessions (one resistant and one susceptible) were inoculated with two *P. capsici* isolates separately. Infected plant tissues were collected at two times after inoculation in three replicates giving 24 biological samples. Samples' total RNAs were extracted and sequenced by the Illumina technology. 37 million paired-end reads were analyzed on average per sample. Between 73.8 and 80.1 % of them mapped to the released *P. capsici* and pepper genomes, with 0.004 to 6.010 % of the mapped paired reads to the reference *P. capsici* gene models and 93.9 to 99.9 % to the pepper transcriptome contigs. Focusing on the pathogen, we observed 5528 genes expressed among the 20 296 *P. capsici* gene models. Comparison analysis between samples highlighted 294 genes with significant differential expression pattern according to the resistance level of the pepper genitors. A preliminary genomic study revealed that some of those genes are involved in pathogenicity. The completion of this study should deliver new tools to aide development of genetic resistance in pepper. This project was supported by Agropolis Fondation under the reference ID « Protéines pathogènes » 1300-002, and by INRA-DBAP under the reference ID « EffeCaps ».